File Copy

RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
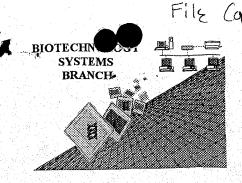BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

RECEIVED

Application Serial Number: *09/446,089A*

MAR 0 5 2001

Source: *1638*

TECH CENTER 1600/2900

Date Processed by STIC: *2/27/2001*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program
employing a logical and intuitive user-interface to check whether a sequence listing is in
compliance with format and content rules. Checker Version 3.0 works for sequence listings
generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old
rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual
Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-
compliant. Checker allows public users to check sequence listings in Computer Readable form
(CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence
listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

●●Sequence Listing Error ●●nary

ERROR DETECTED   SUGGESTED CORRECTION   SERIAL NUMBER: _09/446,089A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 ✓ Use of <220>Feature (NEW RULES)
Sequence(s) /____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/446,089A

DATE: 02/27/2001
TIME: 14:31:44

P. 6

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\02272001\I446089A.raw

```
 3  <110> APPLICANT: SAKAKIBARA, Keiko
 4        FUKUI, Yuko
 5        TANAKA, Yoshikazu
 6        KUSUMI, Takaaki
 7        MIZUTANI, Masako
 8        NAKAYAMA, Toru
10  <120> TITLE OF INVENTION: GENE ENCODING PROTEIN HAVING AURONE SYNTHESIZING ACTIVITY
12  <130> FILE REFERENCE: 001560-377
14  <140> CURRENT APPLICATION NUMBER: US 09/446,089A
15  <141> CURRENT FILING DATE: 1999-12-17
17  <150> PRIOR APPLICATION NUMBER: PCT/JP99/02045
18  <151> PRIOR FILING DATE: 1999-04-16
20  <150> PRIOR APPLICATION NUMBER: JP 10/107296
21  <151> PRIOR FILING DATE: 1998-04-17
23  <160> NUMBER OF SEQ ID NOS: 15
25  <170> SOFTWARE: PatentIn version 3.0
27  <210> SEQ ID NO: 1
28  <211> LENGTH: 1951
29  <212> TYPE: DNA
30  <213> ORGANISM: Antirrhinum majus
32  <220> FEATURE:
33  <221> NAME/KEY: CDS
34  <222> LOCATION: (96)..(1781)
36  <400> SEQUENCE: 1
37  aaattacatt gcttcctttg tcccaccttc caccaccaat atatacaact tcctcagcta        60
39  gttgtttatt atcaatcaaa taaaattatt tccca atg ttc aaa aat cct aat        113
40                                       Met Phe Lys Asn Pro Asn
41                                        1               5
43  atc cgc tat cac aaa cta tct tcc aaa tcc aat gac aac gat caa gaa        161
44  Ile Arg Tyr His Lys Leu Ser Ser Lys Ser Asn Asp Asn Asp Gln Glu
45          10              15              20
47  tcc tcc cat cgt tgt aag cac att cta tta ttt ata ata acc tta ttc        209
48  Ser Ser His Arg Cys Lys His Ile Leu Leu Phe Ile Ile Thr Leu Phe
49          25              30              35
51  cta ctt ata gtt ggc ctg tac atc gcc aac tct ctc gcc tat gcc cgg        257
52  Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn Ser Leu Ala Tyr Ala Arg
53          40              45              50
55  ttt gcc tcg acc tca acc ggc cct atc gcc gcc cct gat gtc acc aaa        305
56  Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala Ala Pro Asp Val Thr Lys
57  55              60              65              70
59  tgt ggt cag cca gac ttg cca cct ggc aca gcc cca ata aac tgt tgt        353
60  Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr Ala Pro Ile Asn Cys Cys
61              75              80              85
63  ccc cca atc ccc gct aaa atc atc gat ttc gag cta cca cct ccc tcc        401
64  Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe Glu Leu Pro Pro Pro Ser
65              90              95              100
67  act acc atg agg gtt cgc cgt gcg gct cat tta gtt gat gat gca tac        449
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RAW SEQUENCE LISTING   DATE: 02/27/2001
PATENT APPLICATION: US/09/446,089A   TIME: 14:31:44

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\02272001\I446089A.raw

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68 Thr Thr Met Arg Val Arg Arg Ala Ala His Leu Val Asp Asp Ala Tyr
69         105                 110                 115
71 att gcc aaa ttc aag aaa gcc gtt gag ctt atg cga gct cta cct gag        497
72 Ile Ala Lys Phe Lys Lys Ala Val Glu Leu Met Arg Ala Leu Pro Glu
73     120             125                 130
75 gat gac cct cgt agc ttc aag caa caa gct aac gtc cat tgc gct tac        545
76 Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala Asn Val His Cys Ala Tyr
77 135             140                 145                 150
79 tgc gcg ggg gcg tat aat caa gcc ggt ttc aca aac cta aag ctc caa        593
80 Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe Thr Asn Leu Lys Leu Gln
81             155                 160                 165
83 atc cac cga tct tgg ctt ttt ttc ccg ttc cat aga tat tat atc tac        641
84 Ile His Arg Ser Trp Leu Phe Phe Pro Phe His Arg Tyr Tyr Ile Tyr
85         170                 175                 180
87 ttt ttt gaa aga ata ttg gga aaa cta atc aat gat aca act ttt gct        689
88 Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile Asn Asp Thr Thr Phe Ala
89         185                 190                 195
91 ctc caa ttt tgg aac tat gat tca cct ggt gga atg aca atc cca tca        737
92 Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly Gly Met Thr Ile Pro Ser
93     200                 205                 210
95 atg ttt att gat act aat tct tcg ctg tac gat agt tta cgg gac agt        785
96 Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr Asp Ser Leu Arg Asp Ser
97 215                 220                 225                 230
99 aat cat cag cca cca acc atc gta gac ttg aac tac gcc ttt tct gat        833
100 Asn His Gln Pro Pro Thr Ile Val Asp Leu Asn Tyr Ala Phe Ser Asp
101             235                 240                 245
103 tcc gac aat acc act act cct gaa gag caa atg att ata aac ctt aaa       881
104 Ser Asp Asn Thr Thr Thr Pro Glu Glu Gln Met Ile Ile Asn Leu Lys
105             250                 255                 260
107 att gtg tac aga caa atg gtg tcg agc gct aag act cca cag ctt ttc       929
108 Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys Thr Pro Gln Leu Phe
109         265                 270                 275
111 ttc ggc cgc cca tac cga cgt ggg gac caa gag ttt ccc ggg gtg ggg      977
112 Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly
113     280                 285                 290
115 tcg att gag tta gtc cct cat ggc atg ata cat tta tgg acc ggt tct      1025
116 Ser Ile Glu Leu Val Pro His Gly Met Ile His Leu Trp Thr Gly Ser
117 295                 300                 305                 310
119 gag aac acg ccc tat ggc gag aac atg ggg gct ttc tac tca acg gct      1073
120 Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly Ala Phe Tyr Ser Thr Ala
121             315                 320                 325
123 aga gac ccg ata ttt ttt gct cat cat tcg aac gtc gat aga atg tgg      1121
124 Arg Asp Pro Ile Phe Phe Ala His His Ser Asn Val Asp Arg Met Trp
125             330                 335                 340
127 tcc ata tgg aag acc cta gga ggg ccg cgg agg acg gac tta aca gat      1169
128 Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg Arg Thr Asp Leu Thr Asp
129         345                 350                 355
131 cca gat ttt ctt gat gcg tct ttc gtt ttt tat gac gaa aac gca gag      1217
132 Pro Asp Phe Leu Asp Ala Ser Phe Val Phe Tyr Asp Glu Asn Ala Glu
```

```
133     360                   365                   370
135 atg gtt cgg gtc aag gtt cgg gat tgc tta gat gaa aag aaa cta ggg      1265
136 Met Val Arg Val Lys Val Arg Asp Cys Leu Asp Glu Lys Lys Leu Gly
137 375                   380                   385                   390
139 tac gtt tat caa gat gtg gag att ccg tgg ctc aac act cgt cca aca      1313
140 Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp Leu Asn Thr Arg Pro Thr
141                   395                   400                   405
143 cca aaa gtt tct ccg tct cta ctt aag aaa ttt cat aga aca aac act      1361
144 Pro Lys Val Ser Pro Ser Leu Leu Lys Lys Phe His Arg Thr Asn Thr
145                   410                   415                   420
147 gcc aat ccg aga caa gtt ttt cct gcg ata ctt gac aga gtc tta aaa      1409
148 Ala Asn Pro Arg Gln Val Phe Pro Ala Ile Leu Asp Arg Val Leu Lys
149                   425                   430                   435
151 gtt atc gtg acg agg ccg aag aaa act aga agt agg aaa gaa aag gac      1457
152 Val Ile Val Thr Arg Pro Lys Lys Thr Arg Ser Arg Lys Glu Lys Asp
153     440                   445                   450
155 gag tta gaa gag att tta gtg att gaa ggg att gaa ctg gaa aga gac      1505
156 Glu Leu Glu Glu Ile Leu Val Ile Glu Gly Ile Glu Leu Glu Arg Asp
157 455                   460                   465                   470
159 cac ggg cac gta aaa ttc gac gtt tat att aat gct gac gaa gat gac      1553
160 His Gly His Val Lys Phe Asp Val Tyr Ile Asn Ala Asp Glu Asp Asp
161                   475                   480                   485
163 ctt gcg gtg att tcg ccg gag aat gct gag ttc gcc ggg agt ttc gtg      1601
164 Leu Ala Val Ile Ser Pro Glu Asn Ala Glu Phe Ala Gly Ser Phe Val
165                   490                   495                   500
167 agt ctg tgg cac aaa cct ata aag ggg aag agg aca aag acg cag tta      1649
168 Ser Leu Trp His Lys Pro Ile Lys Gly Lys Arg Thr Lys Thr Gln Leu
169     505                   510                   515
171 tta aca ttg tcg att tgt gat att ttg gag gat ttg gat gct gac gaa      1697
172 Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu Asp Leu Asp Ala Asp Glu
173     520                   525                   530
175 gat gat tat gtg ttg gtc act ttg gtt ccg aga aac gcc gga gat gcg      1745
176 Asp Asp Tyr Val Leu Val Thr Leu Val Pro Arg Asn Ala Gly Asp Ala
177 535                   540                   545                   550
179 atc aag att cat aat gtc aag att gag ctt gat ggc taataaattc           1791
180 Ile Lys Ile His Asn Val Lys Ile Glu Leu Asp Gly
181                   555                   560
183 tattgatttc ttctcaacct acagttgatc atttaccgat tgattattcc aataaaagta    1851
185 tctcatgtac caatatcgat cgtattaatc gtaatacttt cagatttta tttatttaaa     1911
187 agcagttgta taaatggtga aataaggatt actttttgag                          1951
190 <210> SEQ ID NO: 2
191 <211> LENGTH: 562
192 <212> TYPE: PRT
193 <213> ORGANISM: Antirrhinum majus
195 <400> SEQUENCE: 2
197 Met Phe Lys Asn Pro Asn Ile Arg Tyr His Lys Leu Ser Ser Lys Ser
198 1                   5                   10                  15
201 Asn Asp Asn Asp Gln Glu Ser Ser His Arg Cys Lys His Ile Leu Leu
202                   20                   25                   30
```

```
205 Phe Ile Ile Thr Leu Phe Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn
206           35                40                45
209 Ser Leu Ala Tyr Ala Arg Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala
210      50                55                60
213 Ala Pro Asp Val Thr Lys Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr
214 65                70                75                80
217 Ala Pro Ile Asn Cys Cys Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe
218               85                90                95
221 Glu Leu Pro Pro Pro Ser Thr Thr Met Arg Val Arg Arg Ala Ala His
222           100               105               110
225 Leu Val Asp Asp Ala Tyr Ile Ala Lys Phe Lys Lys Ala Val Glu Leu
226           115               120               125
229 Met Arg Ala Leu Pro Glu Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala
230      130               135               140
233 Asn Val His Cys Ala Tyr Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe
234 145               150               155               160
237 Thr Asn Leu Lys Leu Gln Ile His Arg Ser Trp Leu Phe Phe Pro Phe
238               165               170               175
241 His Arg Tyr Tyr Ile Tyr Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile
242           180               185               190
245 Asn Asp Thr Thr Phe Ala Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly
246           195               200               205
249 Gly Met Thr Ile Pro Ser Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr
250      210               215               220
253 Asp Ser Leu Arg Asp Ser Asn His Gln Pro Pro Thr Ile Val Asp Leu
254 225               230               235               240
257 Asn Tyr Ala Phe Ser Asp Ser Asp Asn Thr Thr Thr Pro Glu Glu Gln
258               245               250               255
261 Met Ile Ile Asn Leu Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala
262           260               265               270
265 Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln
266           275               280               285
269 Glu Phe Pro Gly Val Gly Ser Ile Glu Leu Val Pro His Gly Met Ile
270      290               295               300
273 His Leu Trp Thr Gly Ser Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly
274 305               310               315               320
277 Ala Phe Tyr Ser Thr Ala Arg Asp Pro Ile Phe Phe Ala His His Ser
278               325               330               335
281 Asn Val Asp Arg Met Trp Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg
282           340               345               350
285 Arg Thr Asp Leu Thr Asp Pro Asp Phe Leu Asp Ala Ser Phe Val Phe
286           355               360               365
289 Tyr Asp Glu Asn Ala Glu Met Val Arg Val Lys Val Arg Asp Cys Leu
290      370               375               380
293 Asp Glu Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp
294 385               390               395               400
297 Leu Asn Thr Arg Pro Thr Pro Lys Val Ser Pro Ser Leu Leu Lys Lys
298           405               410               415
301 Phe His Arg Thr Asn Thr Ala Asn Pro Arg Gln Val Phe Pro Ala Ile
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RAW SEQUENCE LISTING   DATE: 02/27/2001
PATENT APPLICATION: US/09/446,089A   TIME: 14:31:44

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\02272001\I446089A.raw

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302              420              425              430
305 Leu Asp Arg Val Leu Lys Val Ile Val Thr Arg Pro Lys Lys Thr Arg
306         435              440              445
309 Ser Arg Lys Glu Lys Asp Glu Leu Glu Glu Ile Leu Val Ile Glu Gly
310     450              455              460
313 Ile Glu Leu Glu Arg Asp His Gly His Val Lys Phe Asp Val Tyr Ile
314 465              470              475              480
317 Asn Ala Asp Glu Asp Asp Leu Ala Val Ile Ser Pro Glu Asn Ala Glu
318             485              490              495
321 Phe Ala Gly Ser Phe Val Ser Leu Trp His Lys Pro Ile Lys Gly Lys
322         500              505              510
325 Arg Thr Lys Thr Gln Leu Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu
326         515              520              525
329 Asp Leu Asp Ala Asp Glu Asp Asp Tyr Val Leu Val Thr Leu Val Pro
330     530              535              540
333 Arg Asn Ala Gly Asp Ala Ile Lys Ile His Asn Val Lys Ile Glu Leu
334 545              550              555              560
337 Asp Gly
341 <210> SEQ ID NO: 3
342 <211> LENGTH: 13
343 <212> TYPE: PRT
344 <213> ORGANISM: Antirrhinum majus
346 <400> SEQUENCE: 3
348 Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro
349 1               5              10
352 <210> SEQ ID NO: 4
353 <211> LENGTH: 12
354 <212> TYPE: PRT
355 <213> ORGANISM: Antirrhinum majus
357 <400> SEQUENCE: 4
359 Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys
360 1               5              10
362 <210> SEQ ID NO: 5
363 <211> LENGTH: 18
364 <212> TYPE: PRT
365 <213> ORGANISM: Antirrhinum majus
367 <400> SEQUENCE: 5
369 Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln
370 1               5              10              15
372 Glu Phe
375 <210> SEQ ID NO: 6
376 <211> LENGTH: 29
377 <212> TYPE: PRT
378 <213> ORGANISM: Antirrhinum majus
380 <220> FEATURE:
381 <221> NAME/KEY: UNSURE
382 <222> LOCATION: (9)..(9)
383 <223> OTHER INFORMATION: Amino acid 9 is Xaa wherein Xaa = unknown or other.
385 <220> FEATURE:
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```
<210>  10
<211>  6
<212>  PRT
<213>  Artificial Sequence
```

See item 12 on Error Summary Sheet

```
<400>  10

His Ala Val Cys Asn Glu
1               5
```

FYI

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\02272001\I446089A.raw

```
L:392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:458 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:466 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:466 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:514 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
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